

## ***rnf220a*<sup>sdu24/+</sup> (CZRC catalog ID: CZ424)**

### **Nature of the mutation**

Between 101 bp to 102 bp of the wild-type *rnf220a* coding sequence, GC is deleted in exon 3. The mutated *rnf220a* codes for a truncated protein containing 251 aa, of which 307 aa are identical to wildtype *rnf220a*.

### **Sense Strand Sequence**

tattctcagtcctatttgggtgtttatgatcacattgattatcccctgtgtctgtcttttcttctgtgctgcagCCC**GGAT**  
**TGGGAAAATGAAGCGC**CGGAAGCCTGAGGATGGACAGGTATGTCCACTGTGCAGCGCCCCG  
CTGGCAGGGACAGAGGAGGAAATGAGTAGGCATGTGGAACAATGTCTGTTCAAGtagcttcat  
gaaccagagatctgggaatccaacctcctctagaaagtttggccttctgcctcaccttccctggacatcagcatctgac  
agacatcagcatctgacaaagcatacacacatacatagatgcaaaaaaatctccttgattactacaactatgttctcc  
tacctgggtgtcc**agggacagttgaaggatta**

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

**atcg** : Forward/Reverse primer

**atcg** : cas9 target site

### **Genotyping assay**

#### **Primers:**

**sdu24\_forward:** 5' tattctcagtcctatttgg 3'

**sdu24\_reverse:** 5' CTGGAGATGGTCAGCGAGTT 3'

#### **PCR program:**

95°C 5min

95°C 30 sec

58°C 30 sec

72°C 30 sec

72°C 8min

4°C hold

} 30 Cycles

**Product size: 408 bp**

## The sequencing results of the CZ424:

CLUSTAL format alignment by MAFFT FFT-NS-i (v7.397)

```
WT          ttctgtgctgcagCCCGGATTGGGAAAATGAAGCCCGGAAGCCTGAGGATGGACAGGTA
sdu24      ttctgtgctgcagCCCGGATTGGGAAAATGAA--CCCGGAAGCCTGAGGATGGACAGGTA
*****
```

## Reference:

None